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Estimation of Genetic Parameters for Economic Traits in Dairy Cattle of Bangladesh

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Abstract: This study was aimed to access information on genetic parameters i.e., heritability and genetic correlations of some economic traits of dairy cattle available in Bangladesh. For that, data materials were collected from Central Cattle Breeding Station and Dairy Farm, Savar, Dhaka recorded during 1992 to 2005 on Indigenous called Local, Friesian \times Local (50 F-50% L) and Jersey \times Local (50 J-50% L) cattle covered birth weight, first lactation milk yield, first lactation length and first calving interval. REML estimated heritabilities (h^2) of BW were 0.365, 0.495 and 0.489 in Local, Friesian \times Local and Jersey \times Local cattle, respectively. The same for FLL, FLMY and FCI were 0.486, 0.428 and 0.128 in Local; 0.495, 0.495 and 0.497 in Friesian \times Local cattle and 0.496, 0.499 and 0.496 in Jersey \times Local cattle. The overall estimates were 0.500, 0.497, 0.498 and 0.499, respectively for BW, FLL, FLMY and FCI. The mediums to high estimates for all the traits indicate that the traits studied were largely influenced by additive gene action. Genetic correlations (r_G) of BW with FLL, FLMY and FCI were very low except medium r_G between BW and FCI in Local cattle. The direction of genetic association was positive except negative r_G were between BW and FLMY and BW and FCI in Local cattle. First lactation length was positively genetically correlated with FLMY and FCI in a medium to high magnitudes in all the studied genetic groups. Genetic correlations between FLMY and FCI were medium in Jersey \times Local cattle but low in Local and Friesian \times Local cattle. The overall estimate was also low. The magnitude of REML estimated (co) variance and genetic parameters obtained in the present study were within the published range of estimates. Therefore, these estimates may be used in selection and breeding programmes for dairy cattle development in Bangladesh.

Key words: Genetic parameters, economic traits, dairy cattle

Introduction

Bangladesh possesses a large cattle population (24.5 million heads cattle, FAO, 2004) comprised of Indigenous, exotic and their crosses with Indigenous (ILRI, 2004). There is wide variation in terms of production as well as reproduction among the existing cattle. To enhance their genetic potential, several indiscriminate attempts were undertaken in past few decades but no remarkable responses are observed (Bhuiyan, 1997, 2001). In most of these programmes, scientific procedures for genetic evaluation of breeding animals-an estimate of the merit of an individual's full complement of genes were not followed. But the pre-requisite for estimation of genetic merit of animals is the good estimate of genetic parameters i.e., heritability and genetic correlation. These genetic parameters are essential tool in animal breeding research and in the design and application of practical breeding programme (Koots *et al.*, 1994).

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In Bangladesh although many studies have been carried out on the comparison of phenotypic performances in cattle (Hossain *et al.*, 2002; Uddin, 2001; Hirooka and Bhuiyan, 1995; Udo *et al.*, 1990; Ahmed and Islam, 1987; Rahman *et al.*, 1987), there are very few studies on genetic parameter estimates for economic traits (Bhuiyan, 1999; Hossain *et al.*, 2002). For that matter, accumulated records maintained at the Central Cattle Breeding Station and Dairy Farm, Savar, Dhaka were utilized in the present study to estimate heritability and genetic correlation of four economic traits in dairy cattle.

Materials and Methods

The experimental data were collected from the record sheets maintained at the Central Cattle Breeding Station and Dairy Farm, Savar, Dhaka. Data recorded during the period of 1972 to 1982 were included in this study. Data were taken on Local, Friesian × Local (50 F-50% L) and Jersey × Local (50 J-50% L) genetic groups of cattle born in summer (April to June), rainy (July to September), winter (October to December) and spring (January to March) seasons. Mean and Standard Errors (SE) for the studied traits e.g., Birth Weight (BW), First Lactation Milk Yield (FLMY), First Lactation Length (FLL) and First Calving Interval (FCI) were estimated using SPSS computer program. The differences in means were tested using Least Significant Difference (LSD) method (Ahmed *et al.*, 2003).

Variance and covariance components of the traits were estimated using Restricted Maximum Likelihood (REML) approach by VCE4 computer program (Groeneveld, 1998). For REML analyses an animal model was used keeping year of birth and season of birth as fixed effect. However, for all traits analyses were carried out both within genetic group as well as over the genetic groups i.e. pooled data. The general single trait animal model used to describe the analysed traits was

$$Y = Xb + Za + Wc + e$$

Where, Y is the vector of observation; X, Z and W are the known incidence matrices that associate with levels of b, a and c with Y; b is the unknown vector of year of birth; a is the unknown vector of animal's breeding value; c is the unknown vector of season of birth and e is the vector of residual effects.

Covariance components and genetic correlations among traits were estimated using multi-trait animal model (Groeneveld, 1998) having animals additive genetic merit as only genetic term.

Results and Discussion

Data were collected from a total of 624 animals of which 489 had complete records for phenotypic and genetic studies of the concerned traits. Phenotypic mean, standard errors and mean comparison for the studied traits are presented in Table 1. Table 2 shows the effect of various factors on studied traits. Only data on animals having complete records (pedigree and performance) were used to estimate genetic parameters. The estimated variance components and heritabilities are shown in Table 3. Similarly, estimated covariance components and genetic correlation (s) among traits are presented in Table 4.

Phenotypic Performance

Local cattle had smallest birth weight (BWT) among the studied genetic groups (Table 1). Udo *et al.* (1990) reported similar result (15.6±0.40 kg) for Pabna cattle - an improved variety of Local cattle. Birth weight of Friesian × Local cattle found in the present study was within the range (17.28±0.436 to 23.05±0.32 kg) reported by Hirooka and Bhuiyan (1995) and Nahar *et al.* (1989),

Table 1: Mean±SE for economic traits studied in three different genetic groups of dairy cattle

Traits	Genetic groups			
	Local Mean±SE	Friesian × Local Mean±SE	Jersey × Local Mean±SE	Overall Mean±SE
Birth weight (kg)	15.87±0.44 ^a (75)	20.68±0.18 ^a (318)	18.89±0.24 ^b (176)	19.49±0.15 (569)
First lactation milk yield (kg)	700.07±39.88 ^b (95)	1753.28±90.31 ^a (333)	1492.80±48.28 ^a (179)	1517.01±0.25 (603)
First lactation length (d)	275.25±7.95 ^b (91)	357.60±4.98 ^a (332)	330.78±7.28 ^b (179)	337.18±3.38 (602)
Calving interval (d)	447.94±14.56 (86)	468.72±7.33 (310)	451.35±9.47 (91)	460.51±5.40 (556)

Figures in the parentheses indicate number of observation, Means with different superscripts in the same row differ significantly ($p < 0.05$)

Table 2: Factors influencing the studied traits

Factors	Trait			
Genetic Group	BWT *	FLL**	FLMY**	FCI
Year of Birth	BWT **	FLL**	FLMY**	FCI**
Season of Birth	BWT	FLL*	FLMY	FCI

* $p < 0.05$ and ** $p < 0.01$

Table 3: Estimates of additive genetic variance and heritability for economic traits

Traits	Genotype	Additive genetic variance	Heritability
Birth Weight	Local	4.603	0.365
	Friesian × Local	3.972	0.495
	Jersey × Local	3.370	0.489
	Pooled	4.279	0.500
First Lactation Milk Yield	Local	8673.197	0.428
	Friesian × Local	1470566.351	0.495
	Jersey × Local	159347.211	0.499
	Pooled	909623.691	0.498
First Lactation length	Local	2486.461	0.486
	Friesian × Local	3578.664	0.495
	Jersey × Local	4025.781	0.496
	Pooled	3588.469	0.497
Calving interval	Local	1629.020	0.128
	Friesian × Local	6545.023	0.497
	Jersey × Local	7251.800	0.496
	Pooled	7162.568	0.499

Table 4: Genetic correlations among economic traits

Traits	Genetic correlation			
	Local	F × L	L × J	Pooled
BW and FLMY	-0.041	0.019	0.072	0.030
BW and FLL	0.065	0.015	0.076	0.064
BW and FCI	-0.360	0.013	0.054	0.030
FLMY and FLL	0.065	0.423	0.692	0.412
FLMY and FCI	0.165	0.099	0.307	0.103
FLL and FCI	0.449	0.053	0.395	0.460

Bhuiyan (1999) and Uddin (2001). Whereas Rege *et al.* (1994) found higher BWT for Jersey × Local crossbred than the present study. Mean First Lactation Milk Yield (FLMY) for Local, Friesian × Local and Jersey × Local cattle observed in the present study (Table 1) were almost similar with the results reported by Ahmed and Islam (1987) in Local, Rahman *et al.* (1987) in Friesian × Local and Hossain and Routledge (1982) in Jersey × Local cattle. The Local-Friesian crossbred produced more milk than Local-Jersey crossbred. The average FLL for Local, Friesian × Local and Jersey × Local and for pooled data (Table 1) were more or less similar. Ahmed and Islam (1987) in Local and Friesian × Local cows and Tekade *et al.* (1994) in Jersey crossbred observed nearly similar values for FLL. The average lengths between first and second calving for Local, Friesian × Local and Jersey × Local cattle and for

pooled data were more or less similar (Table 1). Bhuiyan (1999) and Nahar *et al.* (1989) in Local and Friesian \times Local and Rege *et al.* (1994) in Jersey crossbred also reported very similar range of results obtained in the present study.

Birth weight of cattle was found to be significantly affected ($p < 0.01$) by genetic group (Table 2). Hirooka and Bhuiyan (1995) and Bhuiyan *et al.* (1992) also reported similar significant effect ($p > 0.05$) of genetic group on BWT of calf. Likewise genetic group was also important with respect to FLMY and FLL (Hossain *et al.*, 2002; Uddin, 2001; Bhuiyan, 1999; Sultana and Bhuiyan, 1997; Nahar *et al.*, 1989). But FCI not found to be dependent on genetic group. Birth weight as well as subsequent FLMY, FLL and FCI of cows were influenced highly significantly ($p < 0.01$) by year of birth. Similar results were reported by Hirooka and Bhuiyan (1995) and Bhuiyan *et al.* (1992) on BWT and Hossain *et al.* (2002), Uddin (2001), Bhuiyan (1999) and Sultana and Bhuiyan (1997) on FLMY, FLL and FCI. Except FLL season of birth effect was not important ($p > 0.05$) for BWT, FLMY and FCI. Non significant effect of seasonal variation on studied traits may be attributed to similar feeding and management practices followed through the years.

Heritabilities

The estimated h^2 value of BWT obtained analyzing the pooled data was 0.50, which was higher than the estimates obtained within genetic groups (0.365 in Local, 0.495 in Friesian \times Local and 0.489 in Jersey \times Local). Medium to high h^2 of BWT found in the present experiment was within the published range (0.29 \pm 0.14 in Brown Swiss to 0.64 \pm 0.56 in Friesian \times Local) reported by Mandal and Sachdeva (1999), Plasse *et al.* (2002), Akbulut *et al.* (2002) and Bhuiyan (1999). Estimated heritability values of FLMY separately for three genetic groups and pooled data were high. This high h^2 value indicated that FLMY is largely controlled by additive gene action. Medium to high h^2 for FLMY was also reported by Hossain *et al.* (2002), Gaur *et al.* (1999) and Ageeb and Hillers (1991). The h^2 of FLL in studied genetic groups and for pooled data were almost similar. The high h^2 for FLL found in the present study were within the literature range (0.32 \pm 0.51 in Friesian \times Local cows to 0.80 \pm 0.25 in Friesian-Friesian \times Sahiwal crossbred) reported by Bhuiyan (1999), Nanavati *et al.* (1998), Tekade *et al.* (1994) and Gaur *et al.* (1999). The h^2 value of FCI for Local was low whereas the same for Friesian \times Local, Jersey \times Local and pooled data were high (Table 3). But nearly zero to high h^2 (0.0034 \pm 0.07 in Sahiwal to 0.65 \pm 0.21 in Friesian) of FCI was reported by different authors (Sethi *et al.*, 1997; Gogoi *et al.*, 1992; Bhoite *et al.*, 1999; Gaur *et al.*, 1999). Low h^2 for FCI in Local cattle is important in decision making to the breeder that for improvement of calving efficiency emphasis need to be given on management practices. One possible reason for low heritability of FCI in Local cattle could be that the pedigrees of the Local cattle were not complete as with other genotypes.

Genetic Correlations

Estimates of genetic correlations (r_G) among the studied quantitative traits of dairy cattle are depicted in Table 4. Estimates of r_G for BW and FLL, BW and FLMY and BW and FCI were very low in all of the studied genetic groups of dairy cattle except medium r_G between BW and FCI in Local cattle. Negative r_G of BW with FLMY and FCI were only in Local cattle indicating that genes influencing BW subsequently retarded FLMY and FCI. Low estimates of the present study indicate that BW of individuals is not so important in selection programme to improve FLL, FLMY or FCI in dairy cattle. Genetic correlations between FLL and FLMY in studied genetic groups of dairy cattle obtained in the present study were within the published range (Katoch and Yadav, 1990; Roy and Katpatal, 1988). The r_G between FLL and FLMY in Jersey cattle reported by them were 0.126 \pm 0.06 and 0.89 \pm 0.07, respectively. Bhuiyan (1999) reported that the r_G between FLL and FCI in Friesian and Friesian \times Local graded cows were 0.19 and 0.14, respectively. Results of the present study were higher for all the three genetic groups. This high genetic correlation between FLMY and

FCI is also interesting to the breeders as lifetime production is associated with calving interval. Genetic correlations between FLMY and FCI obtained in the present study were medium to low for the three genetic groups of dairy cattle. Such medium to low estimates of r_G between these two traits was within the published range for different breeds (Lara *et al.*, 1989; Herbert and Bhatnagar, 1989; Roy and Katpatal, 1988). They reported that r_G between lactation milk yield and calving interval were 0.33 ± 0.30 in Holstein cows, 0.06 ± 0.29 in Karan Swiss cows and 0.10 ± 0.33 in Jersey cows, respectively.

Above all, the differences observed among the estimated phenotypic and genetic parameters with that of others reported elsewhere in the world could be attributed to differences in sample size, genetic groups used, environmental conditions (feeding and management practices), models and procedures employed to estimate parameters and so on. However, since these estimates were found using data on animals maintained under the standard conditions of feeding, management and environmental conditions of Bangladesh, these values may well be used for genetic evaluation of animals at national dairy cattle herd. Moreover, the cattle breeding programme in the country need to be better organized to support scientific animal breeding practices such as individual animal recording, genetic parameter estimation using REML procedure and animal selection based of BLUP based breeding values in order to realize expected genetic improvement in the national herds.

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